



blast 2 Sequences results

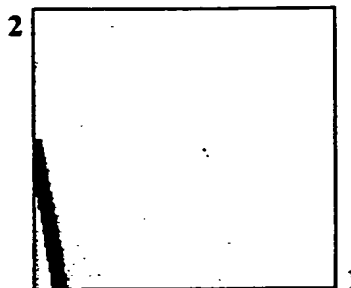
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BLAST 2 SEQUENCES RESULTS VERSION BLASTX 2.1.2 [Nov-13-2000]

Matrix: ☐ gap open: gap extension:
x_dropoff: expect: wordsize: ☒ Filter ☐ Align

Sequence 1 lcl|seq_1 Length 569 (1 .. 569)

Sequence 2 lcl|seq_2 Length 32 (1 .. 32)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 35.4 bits (80), Expect = 0.57
Identities = 16/17 (94%), Positives = 16/17 (94%)
Frame = -1

Query: 53 HWEEAQISRAVLSPPRI 3
HWEEAQISRAVLS PRI
Sbjct: 2 HWEEAQISRAVLSLPRI 18

CPU time: 0.06 user secs. 0.03 sys. secs 0.09 total secs.

Gapped

Lambda	K	H
0.318	0.135	0.401

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 204

Number of Sequences: 0

Number of extensions: 7

Number of successful extensions: 1

Number of sequences better than 10.0: 2

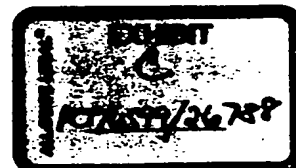
Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 189



length of database: 190,211,578
effective HSP length: 52
effective length of query: 137
effective length of database: 172,828,498
effective search space: 23677504226
effective search space used: 23677504226
frameshift window, decay const: 50, 0.1
T: 9
A: 40
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 69 (31.2 bits)